BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (64 letters)

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BLASTN 2.2.18 (Mar-02-2008)

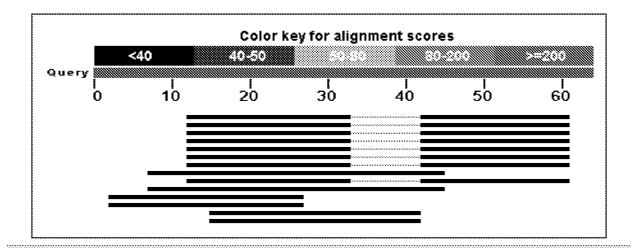
Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 1HASZE0V012 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters



Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= Length=64

Distribution of 22 Blast Hits on the Query Sequence



Distance tree of results MER

Legend for links to other resources: Will UniGene GEO Gene Structure

Sequences producing significant alignments: (Click headers to sort columns)

ıra	anscripts	
MM	0010801	1

папоопра		
NM_001080125.1	Homo sapiens caspase 8, apoptosis- related cysteine peptidase (CASP8), transcript variant G, mRNA	39.2 74.7 62% 0.32 100%
NM_001080124.1	Homo sapiens caspase 8, apoptosis- related cysteine peptidase (CASP8), transcript variant F, mRNA	39.2 74.7 62% 0.32 100%
NM_033358.3	Homo sapiens caspase 8, apoptosis- related cysteine peptidase (CASP8), transcript variant E, mRNA	39.2 74.7 62% 0.32 100%
NM_033356.3	Homo sapiens caspase 8, apoptosis- related cysteine peptidase (CASP8), transcript variant C, mRNA	39.2 74.7 62% 0.32 100%
NM_001228.4	Homo sapiens caspase 8, apoptosis- related cysteine peptidase (CASP8), transcript variant A, mRNA	39.2 74.7 62% 0.32 100%
NM_033355.3	Homo sapiens caspase 8, apoptosis- related cysteine peptidase (CASP8), transcript variant B, mRNA	39.2 74.7 62% 0.32 100%

Genomic sequences [show first]

	t j					
NW_001838863.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188396)	39.2	74.7	62%	0.32	100%
NW_001839136.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188253)	39.2	39.2	59%	0.32	84%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	39.2	74.7	62%	0.32	100%
NT_008046.15	Homo sapiens chromosome 8 genomic contig, reference assembly	39.2	39.2	59%	0.32	84%
NW_001838084.2	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188152)	37.4	37.4	39%	1.1	92%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	37.4	37.4	39%	1.1	92%
NW_001842360.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188416)	35.6	35.6	42%	3.9	88%
NT_011757.15	Homo sapiens chromosome X genomic contig, reference assembly	35.6	35.6	42%	3.9	88%

Alignments

```
>ref|NM 001080125.1| ...... Homo sapiens caspase 8, apoptosis-related cysteine pe
(CASP8), transcript variant G, mRNA Length=2938
GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase [Homo sapiens] (Over 100 PubMed links)
                                                             Sort alignments for this
                                                               E value Score Percen
                                                               Query start position
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
            AAGTTCCTGAGCCTGGACTAC
Query 13
             AAGTTCCTGAGCCTGGACTAC
Sbjct 445
                                     465
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
Query 43
            GTAGTCCAGGCTCAGGAAC 61
             Sbjct 465
            GTAGTCCAGGCTCAGGAAC
(CASP8), transcript variant F, mRNA
Length=2750
GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase [Homo sapiens] (Over 100 PubMed links)
                                                             Sort alignments for this
                                                               E value Score Percen
                                                               Query start position
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
Query 13
            AAGTTCCTGAGCCTGGACTAC
                                     33
             AAGTTCCTGAGCCTGGACTAC
Sbjct 302
                                     322
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
Query 43
            GTAGTCCAGGCTCAGGAAC 61
             GTAGTCCAGGCTCAGGAAC
Sbjct 322
>ref|NM_033358.3| Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant E, mRNA
Length=1123
```

```
GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase [Homo sapiens] (Over 100 PubMed links)
                                                                   Sort alignments for this
                                                                     E value Score Percen
                                                                     Query start position
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
            AAGTTCCTGAGCCTGGACTAC 33
Query 13
              Sbjct 370 AAGTTCCTGAGCCTGGACTAC 390
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
Query 43
              GTAGTCCAGGCTCAGGAAC 61
              Sbjct 390 GTAGTCCAGGCTCAGGAAC
>ref[NM_033356.3] Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant C, mRNA
Length=2655
GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase [Homo sapiens] (Over 100 PubMed links)
                                                                  Sort alignments for this
                                                                     E value Score Percen
                                                                     Query start position
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
              AAGTTCCTGAGCCTGGACTAC 33
Query 13
              Sbjct 207 AAGTTCCTGAGCCTGGACTAC
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
              GTAGTCCAGGCTCAGGAAC 61
Query 43
              Sbjct 227 GTAGTCCAGGCTCAGGAAC
>ref|NM_001228.4| Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant A, mRNA
Length=2914
GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase [Homo sapiens] (Over 100 PubMed links)
                                                                   Sort alignments for this
                                                                     E value Score Percen
                                                                     Query start position
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
```

```
AAGTTCCTGAGCCTGGACTAC
Query 13
             Sbjct 370
            AAGTTCCTGAGCCTGGACTAC
                                      390
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
Query 43
             GTAGTCCAGGCTCAGGAAC
             Sbjct 390 GTAGTCCAGGCTCAGGAAC
>ref|NM_033355.3| Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant B, mRNA
Length=2769
GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase [Homo sapiens] (Over 100 PubMed links)
                                                              Sort alignments for this
                                                                E value Score Percen
                                                                Query start position
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
Query 13
             AAGTTCCTGAGCCTGGACTAC
             AAGTTCCTGAGCCTGGACTAC
Sbjct 276
                                      296
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
Query 43
             GTAGTCCAGGCTCAGGAAC
             Sbjct 296 GTAGTCCAGGCTCAGGAAC
>ref|NW_001838863.1|Hs2_WGA256_36 Momo sapiens chromosome 2 genomic contig, al
(based on HuRef SCAF_1103279188396)
Length=44081246
                                                              Sort alignments for this
                                                                E value Score Percen
                                                                Query start position
 Features in this part of subject sequence:
   caspase 8 isoform G precursor
   caspase 8 isoform E
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
                  AAGTTCCTGAGCCTGGACTAC
Query 13
Sbjct 27538620 AAGTTCCTGAGCCTGGACTAC
                                           27538640
 Features in this part of subject sequence:
   caspase 8 isoform G precursor
   caspase 8 isoform E
```

```
Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
                   GTAGTCCAGGCTCAGGAAC
Query 43
Sbjct 27538640 GTAGTCCAGGCTCAGGAAC
                                         27538622
>ref|NW_001839136.1|Hs8_WGA529_36 Memo sapiens chromosome 8 genomic contig, al
(based on HuRef SCAF_1103279188253)
Length=44702525
 Features in this part of subject sequence:
   hypothetical protein
 Score = 39.2 bits (42), Expect = 0.32 Identities = 32/38 (84%), Gaps = 1/38 (2%)
 Strand=Plus/Plus
                   CCAAAAAGTTCCTGAGCCTGGACTACTCTCTTGAAGTA
Query 8
Sbjct 22623652 CCATAAAGTTACTGAGCCTGGA-TACTCTCCTAAATTA
                                                               22623688
>ref|NT_005403.16|Hs2_5560 Memory Homo sapiens chromosome 2 genomic contig, reference
Length=84213157
                                                                Sort alignments for this
                                                                  E value Score Percen
                                                                  Query start position
 Features in this part of subject sequence:
   caspase 8 isoform G precursor
   caspase 8 isoform E
 Score = 39.2 bits (42), Expect = 0.32 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus
                   AAGTTCCTGAGCCTGGACTAC
Query 13
Sbjct 52340693 AAGTTCCTGAGCCTGGACTAC
                                            52340713
 Features in this part of subject sequence:
   caspase 8 isoform G precursor
   caspase 8 isoform E
 Score = 35.6 bits (38), Expect = 3.9 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
                   GTAGTCCAGGCTCAGGAAC 61
Query 43
                   Sbjct 52340713 GTAGTCCAGGCTCAGGAAC 52340695
>ref|NT_008046.15|Hs8_8203 MM Homo sapiens chromosome 8 genomic contig, reference
Length=57155273
 Features in this part of subject sequence:
   hypothetical protein
 Score = 39.2 bits (42), Expect = 0.32 Identities = 32/38 (84%), Gaps = 1/38 (2%)
 Strand=Plus/Plus
Query 8
                  CCAAAAAGTTCCTGAGCCTGGACTACTCTCTTGAAGTA 45
```

```
Sbjct 22578869
(based on HuRef SCAF_1103279188152)
Length=25468656
Features flanking this part of subject sequence:
   377332 bp at 5' side: hypothetical protein LOC728215
   129111 bp at 3' side: similar to hCG1639781
Score = 37.4 bits (40), Expect = 1.1 Identities = 23/25 (92%), Gaps = 0/25 (0%)
Strand=Plus/Plus
Query 3
               CTTTTCCAAAAAGTTCCTGAGCCTG 27
                Sbjct 4921049 CTTTACCAAATAGTTCCTGAGCCTG
>ref|NT 009952.14|Hs13 10109 🗱 Homo sapiens chromosome 13 genomic contig, refere
Length=25443670
Features flanking this part of subject sequence: 225344 bp at 5' side: arginine and glutamate rich 1
   377210 bp at 3' side: hypothetical protein LOC728215
Score = 37.4 bits (40), Expect = 1.1
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
                CTTTTCCAAAAAGTTCCTGAGCCTG 27
Query 3
                Sbjct 20535311 CTTTACCAAATAGTTCCTGAGCCTG 20535287
>ref|NW_001842360.1|HsX_WGA1321_36 💹 Homo sapiens chromosome X genomic contig, a
(based on HuRef SCAF_1103279188416)
Length=28681338
Features in this part of subject sequence:
  protein phosphatase with EF hand calcium-binding domain 1...
   protein phosphatase with EF hand calcium-binding domain 1...
Score = 35.6 bits (38), Expect = 3.9 Identities = 24/27 (88%), Gaps = 0/27 (0%)
Strand=Plus/Minus
Query 16
                TTCCTGAGCCTGGACTACTCTTTGAA
               Sbjct 10286062
                                            10286036
>ref|NT_011757.15|HsX_11914 W Homo sapiens chromosome X genomic contig, referenc
Length=34879939
Features in this part of subject sequence: protein phosphatase with EF hand calcium-binding domain 1...
   protein phosphatase with EF hand calcium-binding domain 1...
Score = 35.6 bits (38), Expect = 3.9 Identities = 24/27 (88%), Gaps = 0/27 (0%)
Strand=Plus/Minus
                TTCCTGAGCCTGGACTACTCTCTTGAA 42
Query 16
                 Sbjct 16522474 TTCCTGAGCCTGGAATAGTCTCTGGAA 16522448
```

```
Database: human build 36.3 reference assembly genomic scaffolds
    Posted date: Apr 16, 2008 7:40 PM
  Number of letters in database: 1,523,044,440
  Number of sequences in database: 49,942
Lambda
         K
   0.634 0.408
                    0.912
Gapped
Lambda
   0.634 0.408
                    0.912
Matrix: blastn matrix:2 - 3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 49942
Number of Hits to DB: 437151
Number of extensions: 24062
Number of successful extensions: 152
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 152
Number of HSP's successfully gapped: 0
Length of query: 64
Length of database: 5818011736
Length adjustment: 30
Effective length of query: 34
Effective length of database: 5816513476
Effective search space: 197761458184
Effective search space used: 197761458184
A: 0
X1: 22 (20.1 bits)
X2: 33 (29.8 bits)
X3: 110 (99.2 bits)
S1: 30 (28.3 bits)
S2: 37 (34.6 bits)
```